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RAW SEQUENCE LISTING

DATE: 01/09/2002

PATENT APPLICATION: US/09/963,668B

TIME: 14:39:35

Input Set : A:\211283ms.app

Output Set: N:\CRF3\01082002\I963668B.raw

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3 <110> APPLICANT: RIEPING, MECHTHILD
 4 BASTUCK, CHRISTINE
 5 HERMANN, THOMAS
 6 THIERBACH, GEORG
 8 <120> TITLE OF INVENTION: FERMENTATIVE PROCESS FOR THE PREPARATION OF L-AMINO ACIDS
 9 USING STRAINS OF THE FAMILY ENTEROBACTERIACEAE
 11 <130> FILE REFERENCE: 21123/283665/MAS
 13 <140> CURRENT APPLICATION NUMBER: 09/963,668B
 14 <141> CURRENT FILING DATE: 2001-09-27
 16 <150> PRIOR APPLICATION NUMBER: DE 100 48 605.3
 17 <151> PRIOR FILING DATE: 2000-09-30
 19 <150> PRIOR APPLICATION NUMBER: DE 100 55 516.0
 20 <151> PRIOR FILING DATE: 2000-11-09
 22 <150> PRIOR APPLICATION NUMBER: DE 101 30 192.8
 23 <151> PRIOR FILING DATE: 2001-06-22
 25 <160> NUMBER OF SEQ ID NOS: 19
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 1623
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Escherichia coli
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (1)..(1620)
 37 <223> OTHER INFORMATION: pckA
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 42 1 5 10 15
 44 atc agt gac gta cat gat atc gtt tac aac cca agc tac gac ctg ctg 96
 45 Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
 46 20 25 30
 48 tat cag gaa gag ctc gat ccg agc ctg aca ggt tat gag cgc ggg gtg 144
 49 Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
 50 35 40 45
 52 tta act aat ctg ggt gcc gtt gcc gtc gat acc ggg atc ttc acc ggt 192
 53 Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
 54 50 55 60
 56 cgt tca cca aaa gat aag tat atc gtc cgt gac gat acc act cgc gat 240
 57 Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
 58 65 70 75 80
 60 act ttc tgg tgg gca gac aaa ggc aaa ggt aag aac gac aac aaa cct 288
 61 Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
 62 85 90 95
 64 ctc tct ccg gaa acc tgg cag cat ctg aaa ggc ctg gtg acc agg cag 336
 65 Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
 66 100 105 110

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68 ctt tcc ggc aaa cgt ctg ttc gtt gtc gac gct ttc tgt ggt gcg aac 384
69 Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
70      115      120      125
73 ccg gat act cgt ctt tcc gtc cgt ttc atc acc gaa gtg gcc tgg cag 432
74 Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
75      130      135      140
77 gcg cat ttt gtc aaa aac atg ttt att cgc ccg agc gat gaa gaa ctg 480
78 Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
79 145      150      155      160
81 gca ggt ttc aaa cca gac ttt atc gtt atg aac ggc gcg aag tgc act 528
82 Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
83      165      170      175
85 aac ccg cag tgg aaa gaa cag ggt ctc aac tcc gaa aac ttc gtg gcg 576
86 Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
87      180      185      190
89 ttt aac ctg acc gag cgc atg cag ctg att ggc ggc acc tgg tac ggc 624
90 Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
91      195      200      205
93 ggc gaa atg aag aaa ggg atg ttc tcg atg atg aac tac ctg ctg ccg 672
94 Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
95      210      215      220
97 ctg aaa ggt atc gct tct atg cac tgc tcc gcc aac gtt ggt gag aaa 720
98 Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
99 225      230      235      240
101 ggc gat gtt gcg gtg ttc ttc ggc ctt tcc ggc acc ggt aaa acc acc 768
102 Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
103      245      250      255
105 ctt tcc acc gac ccg aaa cgt cgc ctg att ggc gat gac gaa cac ggc 816
106 Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
107      260      265      270
109 tgg gac gat gac ggc gtg ttt aac ttc gaa ggc ggc tgc tac gca aaa 864
110 Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
111      275      280      285
113 act atc aag ctg tcg aaa gaa gcg gaa cct gaa atc tac aac gct atc 912
114 Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
115      290      295      300
117 cgt cgt gat gcg ttg ctg gaa aac gtc acc gtg cgt gaa gat ggc act 960
118 Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
119 305      310      315      320
121 atc gac ttt gat gat ggt tca aaa acc gag aac acc cgc gtt tct tat 1008
122 Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
123      325      330      335
125 ccg atc tat cac atc gat aac att gtt aag ccg gtt tcc aaa gcg ggc 1056
126 Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
127      340      345      350
129 cac gcg act aag gtt atc ttc ctg act gct gat gct ttc ggc gtg ttg 1104
130 His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
131      355      360      365
134 ccg ccg gtt tct cgc ctg act gcc gat caa acc cag tat cac ttc ctc 1152

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135 Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
136      370      375      380
138 tct ggc ttc acc gcc aaa ctg gcc ggt act gag cgt ggc atc acc gaa 1200
139 Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
140 385      390      395      400
142 ccg acg cca acc ttc tcc gct tgc ttc ggc gcg gca ttc ctg tcg ctg 1248
143 Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
144      405      410      415
146 cac ccg act cag tac gca gaa gtg ctg gtg aaa cgt atg cag gcg gcg 1296
147 His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
148      420      425      430
150 ggc gcg cag gct tat ctg gtt aac act ggc tgg aac ggc act ggc aaa 1344
151 Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
152      435      440      445
154 cgt atc tcg att aaa gat acc cgc gcc att atc gac gcc atc ctc aac 1392
155 Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
156      450      455      460
158 ggt tcg ctg gat aat gca gaa acc ttc act ctg ccg atg ttt aac ctg 1440
159 Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
160 465      470      475      480
162 gcg atc cca acc gaa ctg ccg ggc gta gac acg aag att ctc gat ccg 1488
163 Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
164      485      490      495
166 cgt aac acc tac gct tct ccg gaa cag tgg cag gaa aaa gcc gaa acc 1536
167 Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
168      500      505      510
170 ctg gcg aaa ctg ttt atc gac aac ttc gat aaa tac acc gac acc cct 1584
171 Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro
172      515      520      525
174 gcg ggt gcc gcg ctg gta gcg gct ggt ccg aaa ctg taa 1623
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182 <213> ORGANISM: Escherichia coli
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189      20      25      30
191 Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
192      35      40      45
194 Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
195      50      55      60
197 Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
198 65      70      75      80
200 Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
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203 Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
204      100      105      110
206 Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
207      115      120      125
209 Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
210      130      135      140
212 Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
213 145      150      155      160
215 Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
216      165      170      175
218 Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
219      180      185      190
221 Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
222      195      200      205
224 Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
225      210      215      220
227 Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
228 225      230      235      240
230 Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
231      245      250      255
233 Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
234      260      265      270
236 Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
237      275      280      285
239 Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
240      290      295      300
242 Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
243 305      310      315      320
245 Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
246      325      330      335
248 Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
249      340      345      350
251 His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
252      355      360      365
254 Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
255      370      375      380
257 Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
258 385      390      395      400
260 Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
261      405      410      415
263 His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
264      420      425      430
266 Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
267      435      440      445
269 Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
270      450      455      460
272 Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
273 465      470      475      480
275 Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro

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276          485          490          495
278 Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
279          500          505          510
281 Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro
282          515          520          525
284 Ala Gly Ala Ala Leu Val Ala Ala Gly Pro Lys Leu
285          530          535          540
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292 <213> ORGANISM: Escherichia coli
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297 <223> OTHER INFORMATION: Mutagene DNA
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301 <222> LOCATION: (1)..(35)
302 <223> OTHER INFORMATION: Technical DNA/residues of the polylinker sequence
304 <220> FEATURE:
305 <221> NAME/KEY: misc_feature
306 <222> LOCATION: (36)..(522)
307 <223> OTHER INFORMATION: Part of the 5' region (pck1) of the pckA gene
309 <220> FEATURE:
310 <221> NAME/KEY: misc_feature
311 <222> LOCATION: (523)..(542)
312 <223> OTHER INFORMATION: Technical DNA/residues of the polylinker sequence
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316 <222> LOCATION: (543)..(1105)
317 <223> OTHER INFORMATION: Part of the 3' region (pck2) of the pckA gene
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327 caccaaaaga taagtatatc gtccgtgacg ataccactcg cgatactttc tggtagggcag 180
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330 gtgcgaaccc ggatactcgt ctttcgcgtc gtttcatcac cgaagtggcc tggcaggcgc 360
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332 actttatcgt tatgaacggc gcgaagtgca ctaaccgcga gtggaaagaa cagggtctca 480
333 actccgaaaa cttcgtggcg tttaacctga ccgagcgcat gcaagccgaa ttctgcagat 540
334 cctgaagatg gcaactatcg ctttgatgat ggttcaaaaa ccgagaacac ccgcgtttct 600
335 tatccgatct atcacatcga taacattgtt aagccggttt ccaaagcggg ccacgcgact 660
336 aaggttatct tccgactgc tgatgctttc ggcgtgttgc cgccggtttc tcgcctgact 720
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VERIFICATION SUMMARY

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